

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/806, 419A
Source: IFW16
Date Processed by STIC: 12/15/2006

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 12/15/2006

PATENT APPLICATION: US/10/806,419A

TIME: 10:28:36

Input Set : E:\SequenceListing-10-806419.txt

Output Set: N:\CRF4\12152006\J806419A.raw

3 <110> APPLICANT: Papathanassiu, Adonia
 5 <120> TITLE OF INVENTION: Compositions and Methods for Inhibiting Angiogenesis
 7 <130> FILE REFERENCE: A8448
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/806,419A
 C--> 9 <141> CURRENT FILING DATE: 2004-03-23
 9 <150> PRIOR APPLICATION NUMBER: 09/935,145
 10 <151> PRIOR FILING DATE: 2001-08-22
 12 <150> PRIOR APPLICATION NUMBER: 60/227,152
 13 <151> PRIOR FILING DATE: 2000-08-22
 15 <160> NUMBER OF SEQ ID NOS: 23
 17 <170> SOFTWARE: PatentIn version 3.3
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 24
 21 <212> TYPE: PRT
 22 <213> ORGANISM: Artificial Sequence
 24 <220> FEATURE:
 25 <223> OTHER INFORMATION: Synthetic peptide
 27 <400> SEQUENCE: 1
 29 Phe Gly Lys Arg Glu Gln Ala Glu Glu Glu Arg Tyr Phe Arg Ala Gln
 30 1 5 10 15
 33 Ser Arg Glu Gln Leu Ala Ala Leu
 34 20
 37 <210> SEQ ID NO: 2
 38 <211> LENGTH: 24
 39 <212> TYPE: PRT
 40 <213> ORGANISM: Artificial Sequence
 42 <220> FEATURE:
 43 <223> OTHER INFORMATION: Synthetic peptide
 45 <400> SEQUENCE: 2
 47 Phe Gly Lys Arg Glu Gln Ala Glu Glu Glu Arg Tyr Phe Arg Ala Arg
 48 1 5 10 15
 51 Ala Lys Glu Gln Leu Ala Ala Leu
 52 20
 55 <210> SEQ ID NO: 3
 56 <211> LENGTH: 24
 57 <212> TYPE: PRT
 58 <213> ORGANISM: Artificial Sequence
 60 <220> FEATURE:
 61 <223> OTHER INFORMATION: Synthetic peptide
 63 <400> SEQUENCE: 3
 65 Phe Val Lys Arg Glu Arg Ala Thr Glu Asp Phe Phe Val Arg Gln Arg
 66 1 5 10 15
 69 Glu Lys Glu Gln Leu Arg His Leu

(p8-6)

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70          20
73 <210> SEQ ID NO: 4
74 <211> LENGTH: 22
75 <212> TYPE: PRT
76 <213> ORGANISM: Artificial Sequence
78 <220> FEATURE:
79 <223> OTHER INFORMATION: Synthetic peptide
81 <400> SEQUENCE: 4
83 Gly Met Asp Glu Leu Ser Glu Glu Asp Lys Leu Thr Val Ser Arg Ala
84 1          5          10          15
87 Arg Lys Ile Gln Arg Phe
88          20
91 <210> SEQ ID NO: 5
92 <211> LENGTH: 81
93 <212> TYPE: PRT
94 <213> ORGANISM: Homo sapiens
96 <400> SEQUENCE: 5
98 Gly Ser Asp Gln Ser Glu Asn Val Asp Arg Gly Ala Gly Ser Ile Arg
99 1          5          10          15
102 Glu Ala Gly Gly Ala Phe Gly Lys Arg Glu Gln Ala Glu Glu Glu Arg
103          20          25          30
106 Tyr Phe Arg Ala Gln Ser Arg Glu Gln Leu Ala Ala Leu Lys Lys His
107          35          40          45
110 His Glu Glu Glu Ile Val His His Lys Lys Glu Ile Glu Arg Leu Gln
111          50          55          60
114 Lys Glu Ile Glu Arg His Lys Gln Lys Ile Lys Met Leu Lys His Asp
115 65          70          75          80
118 Asp
122 <210> SEQ ID NO: 6
123 <211> LENGTH: 539
124 <212> TYPE: PRT
125 <213> ORGANISM: Homo sapiens
127 <400> SEQUENCE: 6
129 Met Thr Ser Leu Trp Gly Lys Gly Thr Gly Cys Lys Leu Phe Lys Phe
130 1          5          10          15
133 Arg Val Ala Ala Ala Pro Ala Ser Gly Ala Leu Arg Arg Leu Thr Pro
134          20          25          30
137 Ser Ala Ser Leu Pro Pro Ala Gln Leu Leu Leu Arg Ala Val Arg Arg
138          35          40          45
141 Arg Ser His Pro Val Arg Asp Tyr Ala Ala Gln Thr Ser Pro Ser Pro
142          50          55          60
145 Lys Ala Gly Ala Ala Thr Gly Arg Ile Val Ala Val Ile Gly Ala Val
146 65          70          75          80
149 Val Asp Val Gln Phe Asp Glu Gly Leu Pro Pro Ile Leu Asn Ala Leu
150          85          90          95
153 Glu Val Gln Gly Arg Glu Thr Arg Leu Val Leu Glu Val Ala Gln His
154          100          105          110
157 Leu Gly Glu Ser Thr Val Arg Thr Ile Ala Met Asp Gly Thr Glu Gly
158          115          120          125

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161 Leu Val Arg Gly Gln Lys Val Leu Asp Ser Gly Ala Pro Ile Lys Ile
162      130      135      140
165 Pro Val Gly Pro Glu Thr Leu Gly Arg Ile Met Asn Val Ile Gly Glu
166 145      150      155      160
169 Pro Ile Asp Glu Arg Gly Pro Ile Lys Thr Lys Gln Phe Ala Pro Ile
170      165      170      175
173 His Ala Glu Ala Pro Glu Phe Met Glu Met Ser Val Glu Gln Glu Ile
174      180      185      190
177 Leu Val Thr Gly Ile Lys Val Val Asp Leu Leu Ala Pro Tyr Ala Lys
178      195      200      205
181 Gly Gly Lys Ile Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val
182      210      215      220
185 Leu Ile Met Glu Leu Ile Asn Asn Val Ala Lys Ala His Gly Gly Tyr
186 225      230      235      240
189 Ser Val Phe Ala Gly Val Gly Glu Arg Thr Arg Glu Gly Asn Asp Leu
190      245      250      255
193 Tyr His Glu Met Ile Glu Ser Gly Val Ile Asn Leu Lys Asp Ala Thr
194      260      265      270
197 Ser Lys Val Ala Leu Val Tyr Gly Gln Met Asn Gln Pro Pro Gly Ala
198      275      280      285
201 Arg Ala Arg Val Ala Leu Thr Gly Leu Thr Val Ala Glu Tyr Phe Arg
202      290      295      300
205 Asp Gln Glu Gly Gln Asp Val Leu Leu Phe Ile Asp Asn Ile Phe Arg
206 305      310      315      320
209 Phe Thr Gln Ala Gly Ser Glu Val Ser Ala Leu Leu Gly Arg Ile Pro
210      325      330      335
213 Ser Ala Val Gly Tyr Gln Pro Thr Leu Ala Thr Asp Met Gly Thr Met
214      340      345      350
217 Gln Glu Arg Ile Thr Thr Thr Lys Lys Gly Ser Ile Thr Ser Val Gln
218      355      360      365
221 Ala Ile Tyr Val Pro Ala Asp Asp Leu Thr Asp Pro Ala Pro Ala Thr
222      370      375      380
225 Thr Phe Ala His Leu Asp Ala Thr Thr Val Leu Ser Arg Ala Ile Ala
226 385      390      395      400
229 Glu Leu Gly Ile Tyr Pro Ala Val Asp Pro Leu Asp Ser Thr Ser Arg
230      405      410      415
233 Ile Met Asp Pro Asn Ile Val Gly Ser Glu His Tyr Asp Val Ala Arg
234      420      425      430
237 Gly Val Gln Lys Ile Leu Gln Asp Tyr Lys Ser Leu Gln Asp Ile Ile
238      435      440      445
241 Ala Ile Leu Gly Met Asp Glu Leu Ser Glu Glu Asp Lys Leu Thr Val
242      450      455      460
245 Ser Arg Ala Arg Lys Ile Gln Arg Phe Leu Ser Gln Pro Phe Gln Val
246 465      470      475      480
249 Ala Glu Val Phe Thr Gly His Met Gly Lys Leu Val Pro Leu Lys Glu
250      485      490      495
253 Thr Ile Lys Gly Phe Gln Gln Ile Leu Ala Gly Glu Tyr Asp His Leu
254      500      505      510
257 Pro Glu Gln Ala Phe Tyr Met Val Gly Pro Ile Glu Glu Ala Val Ala

```

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258          515          520          525
261 Lys Ala Asp Lys Leu Ala Glu Glu His Ser Ser
262          530          535
265 <210> SEQ ID NO: 7
266 <211> LENGTH: 22
267 <212> TYPE: PRT
268 <213> ORGANISM: Artificial Sequence
270 <220> FEATURE:
271 <223> OTHER INFORMATION: Synthetic peptide
273 <400> SEQUENCE: 7
275 Ser Leu Gln Asp Ile Ile Ala Ile Leu Gly Met Asp Glu Leu Ser Glu
276 1          5          10          15
279 Glu Asp Lys Leu Thr Cys
280          20
283 <210> SEQ ID NO: 8
284 <211> LENGTH: 378
285 <212> TYPE: DNA
286 <213> ORGANISM: Mus musculus
288 <400> SEQUENCE: 8
289 gaattcgagg tgaasgtggt ggaatctggg ggaggcttag tgaagcctgg agggtccttg      60
291 aaactctcct gtgcagcctc tggattcact ttcagtagct atgccatgtc ttgggttcgc      120
293 cagactccag agaagaggct ggagtgggtc gcatccatta gtagtggtgg tagcacctac      180
295 tatccagaca gtgtgaaggg ccgattcacc atctccagag ataatgccag gaacatcctg      240
297 tacctgcaaa tgagcagtcct gaggtctgag gacacggcca tgtattactg tgcaagaggc      300
299 ctaccatttg cttactgggg ccaagggact ctggctactg tctctgcaga gagtcagtcc      360
301 ttcccaaatg tcagatct
304 <210> SEQ ID NO: 9
305 <211> LENGTH: 372
306 <212> TYPE: DNA
307 <213> ORGANISM: Mus musculus
309 <400> SEQUENCE: 9
310 gagctcgata ttgtgatgac acaatctaca gcttccttag ctgtatctct ggggcagagg      60
312 gccaccatct catgcagggc cagccaaagt gtcagtacat ctagctatag ttatatgcac      120
314 tgggtaccaac agaaaccagg acagccaccc aaactcctca tcaagtatgc atccaaccta      180
316 gaatctgggg tccctgccag gttcagtggc agtgggtctg ggacagactt caccctcaac      240
318 atccatcctg tggaggagga ggatactgca acatattact gtcagcacag ttgggagatt      300
320 ccgctcacgt tcggtgctgg gaccaagctg gagctgaaac gggctgatgc tgcaccaact      360
322 gtatccgcat gc
325 <210> SEQ ID NO: 10
326 <211> LENGTH: 32
327 <212> TYPE: DNA
328 <213> ORGANISM: Artificial Sequence
330 <220> FEATURE:
331 <223> OTHER INFORMATION: PCR primer
334 <220> FEATURE:
335 <221> NAME/KEY: misc_feature
336 <222> LOCATION: (18)..(18)
337 <223> OTHER INFORMATION: n is a, c, g, or t
339 <400> SEQUENCE: 10

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W--> 340 cttccggaat tcsargtnma gctgsagsag tc 32
      343 <210> SEQ ID NO: 11
      344 <211> LENGTH: 35
      345 <212> TYPE: DNA
      346 <213> ORGANISM: Artificial Sequence
      348 <220> FEATURE:
      349 <223> OTHER INFORMATION: PCR primer
      352 <220> FEATURE:
      353 <221> NAME/KEY: misc_feature
      354 <222> LOCATION: (18)..(18)
      355 <223> OTHER INFORMATION: n is a, c, g, or t
      357 <400> SEQUENCE: 11

W--> 358 cttccggaat tcsargtnma gctgsagsag tcwgg 35
      361 <210> SEQ ID NO: 12
      362 <211> LENGTH: 34
      363 <212> TYPE: DNA
      364 <213> ORGANISM: Artificial Sequence
      366 <220> FEATURE:
      367 <223> OTHER INFORMATION: PCR primer
      369 <400> SEQUENCE: 12

      370 cctccggaat tccaggttac tctgaaagwg tstg 34
      373 <210> SEQ ID NO: 13
      374 <211> LENGTH: 32
      375 <212> TYPE: DNA
      376 <213> ORGANISM: Artificial Sequence
      378 <220> FEATURE:
      379 <223> OTHER INFORMATION: PCR primer
      381 <400> SEQUENCE: 13

      382 cttccggaat tcgaggtcca rctgcaacar tc 32
      385 <210> SEQ ID NO: 14
      386 <211> LENGTH: 32
      387 <212> TYPE: DNA
      388 <213> ORGANISM: Artificial Sequence
      390 <220> FEATURE:
      391 <223> OTHER INFORMATION: PCR primer
      393 <400> SEQUENCE: 14

      394 cttccggaat tccaggtcca actvcagcar cc 32
      397 <210> SEQ ID NO: 15
      398 <211> LENGTH: 32
      399 <212> TYPE: DNA
      400 <213> ORGANISM: Artificial Sequence
      402 <220> FEATURE:
      403 <223> OTHER INFORMATION: PCR primer
      405 <400> SEQUENCE: 15

      406 cttccggaat tcgaggtgaa sstggtggaa tc 32
      409 <210> SEQ ID NO: 16
      410 <211> LENGTH: 32
      411 <212> TYPE: DNA
      412 <213> ORGANISM: Artificial Sequence

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 12/15/2006
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:10; N Pos. 18
Seq#:11; N Pos. 18
Seq#:20; Xaa Pos. 3
Seq#:22; Xaa Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13,14
Seq#:23; Xaa Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15

VERIFICATION SUMMARY

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Input Set : E:\SequenceListing-10-806419.txt

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:340 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0

L:358 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0

L:470 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0

L:622 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0

L:712 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0